

1, SEQ ID NO: 19). In helical stems, single base bulges or mismatches are shown by gaps in the arrows. A lower case "a" residue above the human apical loop sequence indicates a polymorphism at position 1125.

BW
On page 5, line 13, please insert the following:

SEQ ID NO: 16 shows a *C. elegans* protein sequence with homology to SEQ ID NO: 1.

SEQ ID NO: 17 shows a *Brugla malayi* protein sequence with homology to SEQ ID NO: 1.

SEQ ID NO: 18 shows a *Oryza sativa* (rice) protein sequence with homology to SEQ ID NO: 1.

SEQ ID NO: 19 shows a partial human glutathione peroxidase (GPX-1) nucleic acid sequence with homology to SEQ ID NOS: 2 and 8.

Please replace pages 1-8 of the sequence listing, with pages 1-12 of the enclosed sequence listing.

Remarks

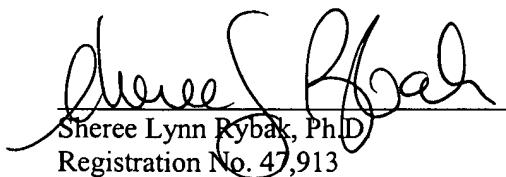
The sequence listing has been amended to include those sequences shown in figures 1-3, and the specification has been amended to denote the SEQ ID NO for the sequences shown in figures 1-3 and to describe SEQ ID NOS 16-19 which were added to the sequence listing. No new matter is added by this amendment, because the sequences added to the sequence listing were present in the original figures as filed.

If there are any questions regarding this amendment, the examiner is invited to telephone the undersigned.

Respectfully submitted,

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By


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**Marked-up Version of Amended Specification
Pursuant to 37 C.F.R. §§ 1.121(b)-(c)**

Replace the paragraphs on page 3, lines 21-37 with the following:

FIG. 1 shows the human cDNA sequence (SEQ ID NO: 2) encoding the 15 kDa selenoprotein and the amino acid sequence (SEQ ID NO: 1) of the selenoprotein itself. In the deduced amino acid sequence, the putative signal peptide is shown in lower case and the most probable site of post-translational cleavage is indicated by an upward arrow. The amino acid U represents selenocysteine 93 encoded by an in-frame TGA codon (overlined). The sequences of four tryptic peptides, for which amino acid sequences were experimentally determined, are underlined. In the 3'-UTR, the positions of the selenocysteine insertion sequence (SECIS element) and the poly-A addition signal (dotted underline) are shown.

FIG. 2 shows alignment of the human 15 kDa selenoprotein sequence (SEQ ID NO: 1) with homologs from mouse (SEQ ID NO: 9), nematodes (C. elegans SEQ ID NO: 16, B. malayi SEQ ID NO: 17) and rice (SEQ ID NO: 18).

FIGS. 3A and 3B relate to the SECIS element. FIG. 3A shows the general features of eukaryotic SECIS elements used to identify a matching element in the 3'-UTRs of the mRNAs encoding human and mouse 15 kDa selenoproteins. FIG. 3B shows an alignment of the predicted SECIS elements of the human (nucleotides 1083-1164 of SEQ ID NO: 2) and mouse mRNAs (nucleotides 1049-1127 of SEQ ID NO: 8) encoding the 15 kDa selenoprotein with a typical experimentally verified example (human GPX-1, SEQ ID NO: 19). In helical stems, single base bulges or mismatches are shown by gaps in the arrows. A lower case "a" residue above the human apical loop sequence indicates a polymorphism at position 1125.

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